

3

RECEIVED

DEC 07 2001

TECH CENTER 1600/2900



1

SEQUENCE LISTING

<110> Gressel, Jonathan
Eyal, Yoram
Fluhr, Robert

<120> RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF

<130> 01/22289

<140> US 09/889,738
<141> 2000-01-20

<150> IL 128193
<151> 1999-01-20

<150> PCT/IL00/00038
<151> 2000-01-20

<160> 21

<170> PatentIn version 3.1

<210> 1
<211> 8
<212> PRT
<213> Citrus X paradisi

<400> 1

Asn Tyr Phe Leu His Leu Thr Ala
1 5

<210> 2
<211> 3
<212> PRT
<213> Citrus X paradisi

<400> 2

Tyr Pro Phe
1

<210> 3
<211> 7
<212> PRT
<213> Citrus X paradisi

<400> 3

Ile Ala Ala Ile Leu Phe Leu
1 5

<210> 4
<211> 8
<212> PRT
<213> Citrus X paradisi

<400> 4

Tyr Phe Pro Ser Leu Met Gly Asn
1 5

<210> 5
<211> 8
<212> PRT
<213> Citrus X paradisi

<400> 5

Glu Lys Met Thr Ile Glu Glu Ala
1 5

<210> 6
<211> 4
<212> PRT
<213> Citrus X paradisi

<400> 6

Leu Phe Gln Pro
1

<210> 7
<211> 14
<212> PRT
<213> Citrus X paradisi

<400> 7

Val Val Asp Asn Gly Met Gly Met Val Val Pro Arg Asp Lys
1 5 10

<210> 8
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (9)..(9)
<223> Modified base : Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> Modified base : Inosine

<400> 8
gayaayggna tgggnatggt

20

<210> 9
<211> 7
<212> PRT
<213> Citrus X paradisi

<400> 9

Asp Asn Gly Met Gly Met Val
1 5

<210> 10
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (12)..(12)
<223> Modified base: Inosine

<400> 10
garaaratga cnathgarga rgc

23

<210> 11
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (12)..(12)
<223> Modified base : Inosine

<220>
<221> misc_feature
<222> (18)..(18)
<223> Modified base : Inosine

<220>
<221> misc_feature
<222> (21)..(21)
<223> Modified base : Inosine

<400> 11
aaytayttyc tncayctnac ngc

23

<210> 12
<211> 8
<212> PRT
<213> Citrus X paradisi

<400> 12

Asn Tyr Phe Leu His Leu Thr Ala
1 5

<210> 13

<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 13
gttttcccgag tcacgacgtt tttttttttt ttt 33

<210> 14
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 14
gttttcccgag tcacgacg 18

<210> 15
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 15
catgccccata ccattgtc 18

<210> 16
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 16
gacaatggta tgggcattg 18

<210> 17
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 17
cctcaaccac cgagccccaa ccac 24

<210> 18
<211> 27
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 18

catctagaat ggataccaaag catcaag

27

<210> 19

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 19

caggatcctt attcagattt cttgacaag

29

<210> 20

<211> 1359

<212> DNA

<213> Citrus X paradisi

<400> 20

atggatacca agcatcaaga taagccaagc attctcatgt taccatggct agtcatggg 60

cacatagctc cacacccctga acttgccaaag aagctttcac agaaaaactt ccacatatat 120

ttctgctcta ctcccaacaa tctacaatcc ttcggcagaa atgttggaaa aaacttctca 180

tcttcataac aactcataga actgcaactt cccatacat tccctgaact tccttcacaa 240

aatcagacca caaaaaaccc ttctccccat cttatttata ctctcggtgg agcattgaa 300

gacgcacaaac ctgcttttg caacatctt gagacgctta aaccaacccct tgttatgtat 360

gatttgttcc aaccgatggc ggcggaggca gcttaccagt atgacatagc tgctatttt 420

ttcttaccct tatctgcagt agcctgctt ttcttgctgc acaatatcgtaa aatcccac 480

ctgaaataacc ctttcttga atctgattac caagatagag aaagcaagaa catcaattac 540

ttcctgcac ttactgccaa tggcacctt aacaaagaca gtttcttaaa agcttgcac 600

ctatcttgcac aatttgcgtt catcaaaaca tcaagagaga ttgaatccaa gtacttggat 660

tatttccctt cttaatggg aaatgaaata attccagtag ggcctctaattt ccaagaaccc 720

accttcaagg tagatgatac aaagatcatg gactggctga gccaaaaggaa gcctcgat 780

gtcgtgtatg catcccttgg cagtggatc tttcccttca cggatgaaat acatgacata 840

gctattgggt tattgctcac cgaggatataat tttatatggg ctttcagatt acatcctgat 900

gagaaaaatga cgatagagga agcactgcct caggccttgg ctgaggagat tgaaaggaat 960

aataaggaa tggatgtaca aggttgggtt ccgcaggcta aaattttaag gcatgaaagc 1020

atcggcggat ttttgcgtca ttgtgggtgg ggctcggtgg ttgaggggat gttttcggtt 1080

gtaccaatca taggtgtgcc aatggcatat gagcagccaa gcaatgccaa ggtgggtgg 1140

gacaatggta tggcatggt cggttccaaaga gataagatca atcaaagact tggaggagag 1200

gaggtggcga gggcattaa acatgttggc ctgcaagaag aagcgaagca aataagaaga 1260

aaagctaatg aaattagtga gagtatgaag aagatagggg acgcacagat gagtgtggtg 1320
 gtggagaaaac tgctgcagct tgtcaagaaa tctgaataa 1359

<210> 21
 <211> 452
 <212> PRT
 <213> Citrus X paradisi

<400> 21

Met Asp Thr Lys His Gln Asp Lys Pro Ser Ile Leu Met Leu Pro Trp
 1 5 10 15

Leu Ala His Gly His Ile Ala Pro His Leu Glu Leu Ala Lys Lys Leu
 20 25 30

Ser Gln Lys Asn Phe His Ile Tyr Phe Cys Ser Thr Pro Asn Asn Leu
 35 40 45

Gln Ser Phe Gly Arg Asn Val Glu Lys Asn Phe Ser Ser Ser Ile Gln
 50 55 60

Leu Ile Glu Leu Gln Leu Pro Asn Thr Phe Pro Glu Leu Pro Ser Gln
 65 70 75 80

Asn Gln Thr Thr Lys Asn Leu Pro Pro His Leu Ile Tyr Thr Leu Val
 85 90 95

Gly Ala Phe Glu Asp Ala Lys Pro Ala Phe Cys Asn Ile Leu Glu Thr
 100 105 110

Leu Lys Pro Thr Leu Val Met Tyr Asp Leu Phe Gln Pro Met Ala Ala
 115 120 125

Glu Ala Ala Tyr Gln Tyr Asp Ile Ala Ala Ile Leu Phe Leu Pro Leu
 130 135 140

Ser Ala Val Ala Cys Ser Phe Leu Leu His Asn Ile Val Asn Pro Ser
 145 150 155 160

Leu Lys Tyr Pro Phe Phe Glu Ser Asp Tyr Gln Asp Arg Glu Ser Lys
 165 170 175

Asn Ile Asn Tyr Phe Leu His Leu Thr Ala Asn Gly Thr Leu Asn Lys
 180 185 190

Asp Arg Phe Leu Lys Ala Phe Glu Leu Ser Cys Lys Phe Val Phe Ile
 195 200 205

Lys Thr Ser Arg Glu Ile Glu Ser Lys Tyr Leu Asp Tyr Phe Pro Ser
210 215 220

Leu Met Gly Asn Glu Ile Ile Pro Val Gly Pro Leu Ile Gln Glu Pro
225 230 235 240

Thr Phe Lys Val Asp Asp Thr Lys Ile Met Asp Trp Leu Ser Gln Lys
245 250 255

Glu Pro Arg Ser Val Val Tyr Ala Ser Phe Gly Ser Glu Tyr Phe Pro
260 265 270

Ser Thr Asp Glu Ile His Asp Ile Ala Ile Gly Leu Leu Leu Thr Glu
275 280 285

Val Asn Phe Ile Trp Ala Phe Arg Leu His Pro Asp Glu Lys Met Thr
290 295 300

Ile Glu Glu Ala Leu Pro Gln Gly Phe Ala Glu Glu Ile Glu Arg Asn
305 310 315 320

Asn Lys Gly Met Ile Val Gln Gly Trp Val Pro Gln Ala Lys Ile Leu
325 330 335

Arg His Gly Ser Ile Gly Gly Phe Leu Ser His Cys Gly Trp Gly Ser
340 345 350

Val Val Glu Gly Met Val Phe Gly Val Pro Ile Ile Gly Val Pro Met
355 360 365

Ala Tyr Glu Gln Pro Ser Asn Ala Lys Val Val Val Asp Asn Gly Met
370 375 380

Gly Met Val Val Pro Arg Asp Lys Ile Asn Gln Arg Leu Gly Gly Glu
385 390 395 400

Glu Val Ala Arg Val Ile Lys His Val Val Leu Gln Glu Ala Lys
405 410 415

Gln Ile Arg Arg Lys Ala Asn Glu Ile Ser Glu Ser Met Lys Lys Ile
420 425 430

Gly Asp Ala Gln Met Ser Val Val Glu Lys Leu Leu Gln Leu Val
435 440 445

Lys Lys Ser Glu
450